

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 01:24:04 ; Search time 25.78 Seconds
(without alignments)
4854.724 Million cell updates/sec

Title: US-09-515-806-2

Perfect score: 1643

Sequence: 1 MAGGRCAPGRGRDEPPESYP.....YNIKVEKKVSVLFLSYRDRD 1643

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	932	56.7	938	2 T46924	probable translati
2	14	0.9	1589	2 T13826	translation initia
3	11	0.7	576	2 S22127	protein kinase pol
4	10	0.6	307	2 S47244	C-rat protein - ze
5	10	0.6	312	2 T32446	hypothetical prote
6	10	0.6	323	1 TVMVF6	protein kinase (EC
7	10	0.6	328	1 TVMSBF	protein kinase B-r
8	10	0.6	380	1 TVFVMM	protein kinase (EC
9	10	0.6	437	1 TVMSRF	protein kinase A-r
10	10	0.6	450	1 TVFVMR	protein kinase (EC
11	10	0.6	462	2 S29851	protein kinase 6 (
12	10	0.6	547	2 S48441	K06H7.1 protein -
13	10	0.6	602	1 TVRTRR	serine/threonine-s
14	10	0.6	603	2 S34130	protein kinase (EC
15	10	0.6	603	2 A47545	protein kinase (EC
16	10	0.6	603	2 A54596	protein kinase A-r
17	10	0.6	604	1 S00726	protein kinase - m
18	10	0.6	606	1 TVHUAF	protein kinase A-r
19	10	0.6	615	2 T29223	hypothetical prote
20	10	0.6	638	1 TVXLRF	protein kinase raf
21	10	0.6	647	1 S00644	protein kinase raf
22	10	0.6	648	1 TVHU6F	protein kinase raf
23	10	0.6	648	1 TVTRBF	protein kinase raf
24	10	0.6	648	2 T43337	protein kinase raf
25	10	0.6	763	1 TVHUBF	polo-like kinase-1
26	10	0.6	781	1 TVFFDF	protein kinase B-r
27	10	0.6	806	1 JN0612	protein kinase Dra
28	10	0.6	807	1 I51153	protein kinase B-r
29	10	0.6	813	1 S33261	protein kinase lin

30	10	0.6	1079	1 TVFVMI	gag-Rml1-env polyp
31	10	0.6	1696	2 T27447	hypothetical prote
32	9	0.5	294	1 DNCHEM	nucleophosmin - ch
33	9	0.5	303	2 A84831	probable protein k
34	9	0.5	339	2 T22168	hypothetical prote
35	9	0.5	402	1 TVFVUR	protein-tyrosine k
36	9	0.5	440	2 T25722	hypothetical prote
37	9	0.5	513	1 S50216	translation initia
38	9	0.5	515	1 A59309	translation initia
39	9	0.5	570	2 T37314	serine/threonine-s
40	9	0.5	607	2 S53387	autoantigen NOR-90
41	9	0.5	620	2 A53731	ribosomal transcri
42	9	0.5	626	2 A41284	
43	9	0.5	683	2 T38254	
44	9	0.5	727	2 S18193	
45	9	0.5	727	2 JC5113	

ALIGNMENTS

RESULT 1

T46924

probable translation initiation factor eIF-2alpha kinase (EC 2.7.1.-) [similarity]
N;Alternate names: hypothetical protein DKFZp434P0612.1
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 20-Jun-2000
C;Accession: T46924; T46325

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, February 2000

A;Reference number: 224138

A;Accession: T46924

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-938 <AAA>

A;Cross-references: EMBL:AL157497

A;Experimental source: adult testis; clone DKFZp434F1312

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A;Reference number: 223035

A;Accession: T46325

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 748-938 <AA2>

A;Cross-references: EMBL:AL137627

A;Experimental source: adult testis; clone DKFZp434P0612

C;Genetics:

A;Note: DKFZp434F1312.1; DKFZp434P0612.1

C;Superfamily: histidine--trNA ligase homology; protein kinase homology

C;Keywords: phosphotransferase

F.1-290/Domain: protein kinase homology (fragment) <KIN>

F.340-747/Domain: histidine--trNA ligase homology <HTL>

Query Match

Best Local Similarity 56.7%; Score 932; DB 2; Length 938;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 STSGERSASARPPATGPGSDDEDDDEHGCVFSQSFSPASDSSEDIIFNEDENSKSQ 771

Db 1 STSGERSASARPPATGPGSDDEDDDEHGCVFSQSFSPASDSSEDIIFNEDENSKSQ 60

QY 772 NDEDCNEKNCHESEPSVTTEAVHYLIQMEYCEKSTLRDTIDGGLYRDTVRLWRLFRE 831

Db 61 NDEDCNEKNCHESEPSVTTEAVHYLIQMEYCEKSTLRDTIDGGLYRDTVRLWRLFRE 120

QY 832 ILDGLAYIHEKGMIRDLKPVNIFLSDSDHVKIGDFGLATDHLAFSADSKODDQTDGLIK 891

Db 121 ILDGLAYIHEKGMIRDLKPVNIFLSDSDHVKIGDFGLATDHLAFSADSKODDQTDGLIK 180

QY 892 SDPSGHLTGMVGTALYVSPVQSGSTKSAYNQKVDLFLSLGIFFEMSYHPMTASERFVL 951

Db 181 SDPSGHLTGMVGTALYVSPVQSGSTKSAYNQKVDLFLSLGIFFEMSYHPMTASERFVL 240

QY 952 NQLRDPSPKPEPDDGGEHAKQSVISWLLNHDPAKRPATATELLKSELLPPQMESEL 1011
DB 241 NQLRDPSPKPEPDDGGEHAKQSVISWLLNHDPAKRPATATELLKSELLPPQMESEL 300
QY 1012 HEVLHPTLTNVGKAYRTMAQIFQSRIAPDIYVDSIDILKGNFSTRAKMOQHVCETI 1071
DB 301 HEVLHPTLTNVGKAYRTMAQIFQSRIAPDIYVDSIDILKGNFSTRAKMOQHVCETI 360
QY 1072 IRIFKRGAVQLCTPLLPNRQIYHEHNEAALFMDHSGMLVLPDLRPFARYVARNNI 1131
DB 361 IRIFKRGAVQLCTPLLPNRQIYHEHNEAALFMDHSGMLVLPDLRPFARYVARNNI 420
QY 1132 LNLKRYCIERVFRPKLDRPHPELLECAFDIVTSTNSPLTAELIYIYIIEQEPAL 1191
DB 421 LNLKRYCIERVFRPKLDRPHPELLECAFDIVTSTNSPLTAELIYIYIIEQEPAL 480
QY 1192 QERNYSYLVNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSLSS 1251
DB 481 QERNYSYLVNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSLSS 540
QY 1252 NSLCRLYKFIEQKGLDQDLPTINSLIKQKTGIAQLVKYKDLFEEVWGLLKGIGIKLQV 1311
DB 541 NSLCRLYKFIEQKGLDQDLPTINSLIKQKTGIAQLVKYKDLFEEVWGLLKGIGIKLQV 600
QY 1312 LINLGLVYKVOHNGIIFQVAFTRKRORAVPEILAAAGRYDILLIPOFRGPQALGPVPTA 1371
DB 601 LINLGLVYKVOHNGIIFQVAFTRKRORAVPEILAAAGRYDILLIPOFRGPQALGPVPTA 660
QY 1372 IGVSTAIIDKISAAVNMEESTVITSSCDLLVYVSGOMSRRAINLTQKLTAGITAEIMYD 1431
DB 661 IGVSTAIIDKISAAVNMEESTVITSSCDLLVYVSGOMSRRAINLTQKLTAGITAEIMYD 720
QY 1432 WSQSOEELQECRHHETIYVALVSDKESGVKVSFKEKQTEKRVLETDLVHVLQKLR 1491
DB 721 WSQSOEELQECRHHETIYVALVSDKESGVKVSFKEKQTEKRVLETDLVHVLQKLR 780
QY 1492 TKVTDNRGRASDNLAVONLKGFSNAGLFEIHGATVVPVIVSVLAPEKLSASTRRYE 1551
DB 781 TKVTDNRGRASDNLAVONLKGFSNAGLFEIHGATVVPVIVSVLAPEKLSASTRRYE 840
QY 1552 TQVQTRLOTSANLHOKSSEIEILLAVDLPKETILOFSLSEWDADQAFNTVKQLLSRLP 1611
DB 841 TQVQTRLOTSANLHOKSSEIEILLAVDLPKETILOFSLSEWDADQAFNTVKQLLSRLP 900
QY 1612 KORYLKLVCDEIYNKVEKVSFLYSYRDD 1643
DB 901 KORYLKLVCDEIYNKVEKVSFLYSYRDD 932

RESULT 2
T13826 translation initiation factor eIF-2 alpha kinase (EC 2.7.1.-) [imported] - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13826; T13060
R:Sanjoto, J.; Alcald, J.; Mendez, R.; Pulido, D.; de Haro, C.
J. Biol. Chem. 272, 12544-12550, 1997
A:Title: Cloning and characterization of a cDNA encoding a protein synthesis initiation factor
A:Reference number: 217783; MUID: 97284729
A:Accession: T13826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1589 <SAN>
A:Cross-references: EMBL:U80223; NID:g2073563; PID:g2073564; PIDN:AAC47516.1
R:Olson, D.S.; Jordan, B.; Chen, D.; Wek, R.C.; Cavanaugh, D.R.
Genetics 149, 1495-1509, 1998
A:Title: Isolation of the gene encoding the Drosophila melanogaster homolog of the Saccharosyl transferase
A:Reference number: 213099; MUID: 98315111
A:Accession: T13060
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-687, 'K', 689-1426, 'H', 1428-1589 <OLS>

A:Cross-references: EMBL:AF056302; NID:g3046550; PID:g3046551; PIDN:AAC13490.1
C:Genetics:
A:Gene: GCN2
A:Cross-references: FlyBase:FBgn0019990
C:Superfamily: histidine--trNA ligase homology; protein kinase homology
C:Keywords: phosphotransferase; protein kinase
F:521-898/Domain: protein kinase homology <KIN>
F:958-1285/Domain: histidine--trNA ligase homology <HTL>

Query Match 0.9%; Score 14; DB 2; Length 1589;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 IHRDLKPVNIFLDS 858
DB 741 IHRDLKPVNIFLDS 754

RESULT 3
S22127 protein kinase polo (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S22127
R:Sunkel, C.E.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22127
A:Accession: S22127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <SUN>
A:Cross-references: EMBL:X63361; NID:g8355; PIDN:CAA44963.1; PID:g8356
C:Genetics:
A:Gene: FlyBase:polo
A:Cross-references: FlyBase:FBgn0003124
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:23-277/Domain: protein kinase homology <KIN>

Query Match 0.7%; Score 11; DB 2; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 HVKIGDFGLAT 871
DB 161 HVKIGDFGLAT 171

RESULT 4
S47244 C-raf protein - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S47244
R:Daniotti, J.L.
submitted to the EMBL Data Library, August 1994
A:Reference number: S47244
A:Accession: S47244
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-307 <DAN>
A:Cross-references: EMBL:X81128; NID:g534976; PIDN:CAA57035.1; PID:g534977
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C:Keywords: ATP
F:7-273/Domain: protein kinase homology <KIN>
F:15-23/Region: protein kinase ATP-binding motif

Query Match 0.6%; Score 10; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
Db 142 VKIGDFGLAT 151

RESULT 5

T32446
hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 03-Nov-2000
C:Accession: T32446
R:Maggi, L.; Harper, M.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid H42K12.
A:Reference number: Z21169
A:Accession: T32446
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-312 <MAG>
A:Cross-references: EMBL:AF026207; PIDN:AAB71265.1; GSPDB:GN00028; CESP:H42K12.1
A:Experimental source: strain Bristol N2; clone H42K12
C:Genetics:
A:Gene: CESP:H42K12.1
A:Map position: X
A:Introns: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 0.6%; Score 10; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 VGTALYVSPE 911
Db 177 VGTALYVSPE 186

RESULT 6

T32446
protein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
N:Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-s
C:Species: murine sarcoma virus 3611
A:Note: host Mus musculus (mouse)
C>Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 23-Feb-1997
C:Accession: A00638; A38020
R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine
A:Reference number: A00638; MUID:84121298
A:Accession: A00638
A:Molecule type: DNA
A:Residues: 1-323 <KAN>
A:Experimental source: ATCC 45010
R:Mark, G.E.; Rapp, U.R.
Science 224, 285-289, 1984
A:Title: Primary structure of v-raf: relatedness to the src family of oncogenes.
A:Reference number: A38020; MUID:84172180
A:Accession: A38020
A:Molecule type: DNA
A:Residues: 1-323 <MAR>
C:Comment: This protein is translated as a gag-raf polypeptide.
C:Genetics:
A:Gene: raf
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase;
F:22-288/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:50/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 862 VKIGDFGLAT 871
Db 157 VKIGDFGLAT 166

RESULT 7

T32446
protein kinase B-raf (EC 2.7.1.1) - mouse (fragment)
N:Alternate names: kinase-related transforming protein B-raf; P94
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1993 #sequence_revision 09-Aug-1996 #text_change 23-Feb-1997
C:Accession: A40951
R:Miki, T.; Fleming, T.P.; Crescenzi, M.; Molloy, C.J.; Blam, S.B.; Reynolds, S.H.; A
Proc. Natl. Acad. Sci. U.S.A. 88, 5167-5171, 1991
A:Title: Development of a highly efficient expression cDNA cloning system: applicatio
A:Reference number: A40951; MUID:91271351
A:Accession: A40951
A:Molecule type: mRNA
A:Residues: 1-328 <MIK>
A:Cross-references: GB:M64429
A:Note: the reported sequence is the product of recombination of TIF1 and B-raf genes
C:Genetics:
A:Gene: B-raf
C:Function:
A:Description: member of signal transduction pathway(s) activated by nerve growth fac
A:Pathway: MAP kinase cascade
A:Note: found in hippocampal neurons and dendritic spines and in high levels in fetal
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:17-283/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:45/Active site: Lys #status predicted
F:169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
Db 152 VKIGDFGLAT 161

RESULT 8

T32446
protein kinase (EC 2.7.1.37) mil - avian myelocytomatosis virus MH2
N:Alternate names: kinase-related transforming protein mil (mht); mil proto-oncogene
C:Species: avian myelocytomatosis virus MH2
A:Note: host Gallus gallus (chicken)
C>Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 23-Feb-1997
C:Accession: A00639; B00638; A21137
R:Sutrave, P.; Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Bister, K.
Nature 309, 85-88, 1984
A:Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine
A:Reference number: A00639; MUID:84191511
A:Accession: A00639
A:Molecule type: DNA
A:Residues: 1-380 <SUT>
A:Cross-references: GB:K02082
A:Note: the authors translated the codon CAG for residue 58 as Gly
R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by mu
A:Reference number: A00638; MUID:84121298
A:Accession: B00638
A:Molecule type: DNA
A:Residues: 1-210, 'E', 212-380 <KAN>
A:Cross-references: GB:K02084
R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984

A:Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, one
 A:Reference number: A21137; MUID:84221892
 A:Accession: A21137
 A:Molecule type: DNA
 A:Residues: 1-210,'E',212-230,'E',232-380 <KA2>
 A:Cross-references: GB:K02082
 C:Comment: This protein is translated as a gag-mht or gag-mil polyprotein.
 C:Genetics:
 A:Gene: mht; mil
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; oncogene; phosphotransferase; polyprotein; serine/threonine-specific pr
 F:80-346/Domain: protein kinase homology <KIN>
 F:88-96/Region: protein kinase ATP-binding motif
 F:108/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0

QY 862 VKIGDFGLAT 871
 |||||
 Db 215 VKIGDFGLAT 224

RESULT 9

TMMSRF
 N:Alternate names: A-raf-1 (EC 2.7.1.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
 C:Accession: A25382
 R:Huleihel, M.; Goldsborough, M.; Cleveland, J.; Gannell, M.; Bonner, T.; Rapp, U.R.
 Mol. Cell. Biol. 6, 2655-2662, 1986
 A:Title: Characterization of murine A-raf, a new oncogene related to the v-raf oncogene.
 A:Reference number: A25382; MUID:87064566
 A:Accession: A25382
 A:Molecule type: mRNA
 A:Residues: 1-437 <HUL>
 A:Cross-references: GB:M13071; NID:gi92016; PIDN:AAA37258.1; PID:g387104
 C:Genetics:
 A:Gene: A-raf
 C:Function:
 A:Description: signal transduction between cell membrane and nucleus; after phosphorylat
 A:Pathway: MAP kinase cascade
 A:Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues
 C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
 F:139-405/Domain: protein kinase homology <KIN>
 F:147-155/Region: protein kinase ATP-binding motif
 F:47/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:56/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
 F:167/Active site: Lys #status predicted
 F:413/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 437;
 Best Local Similarity 100.0%; Pred. No. 0.53; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0

QY 862 VKIGDFGLAT 871
 |||||
 Db 274 VKIGDFGLAT 283

RESULT 10

TFVWVR
 N:Alternate names: Rous-associated virus (type 1)
 C:Species: Rous-associated virus
 A:Note: host Gallus gallus (chicken)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999
 C:Accession: A40341

R:Felder, M.P.; Eychene, A.; Barnier, J.V.; Calogeraki, I.; Calothy, G.; Marx, M.
 J. Virol. 65, 3633-3640, 1991
 A:Title: Common mechanism of retrovirus activation and transduction of c-mil and c-Rn
 A:Reference number: A40341; MUID:91251215
 A:Accession: A40341
 A:Molecule type: DNA
 A:Residues: 1-450 <FEU>
 A:Cross-references: GB:M62407; NID:g210080; PIDN:AAA42549.1; PID:g210081
 C:Comment: This protein is translated as a mil-env polyprotein.
 C:Genetics:
 A:Gene: R-mil
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kina
 F:81-347/Domain: protein kinase homology <KIN>
 F:89-97/Region: protein kinase ATP-binding motif
 F:109/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0

QY 862 VKIGDFGLAT 871
 |||||
 Db 216 VKIGDFGLAT 225

RESULT 11

S29851
 protein kinase 6 (EC 2.7.1.1) - soybean
 C:Species: Glycine max (soybean)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S29851; S27760
 R:Feng, X.H.; Zhao, Y.; Bottino, P.J.; Kung, S.
 Biochim. Biophys. Acta 1172, 200-204, 1993
 A:Title: Cloning and characterization of a novel member of protein kinase family from
 A:Reference number: S29851; MUID:93176812
 A:Accession: S29851
 A:Molecule type: mRNA
 A:Residues: 1-462 <FEN>
 A:Cross-references: EMBL:M67449; NID:q170046; PIDN:AAA34002.1; PID:q170047
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; phosphotransferase
 F:154-419/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 0.56; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0

QY 636 EVTLRLHH 645
 |||||
 Db 207 EVTLRLHH 216

RESULT 12

S44841
 K06H7.1 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S44841
 R:Favello, A.D.
 submitted to the EMBL Data Library, May 1993
 A:Description: Sequence of the C. elegans cosmid K06H7.
 A:Reference number: S44620
 A:Accession: S44841
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-547 <FAV>
 A:Cross-references: EMBL:L15314; NID:g289690; PIDN:AAA28084.1; PID:g289691
 C:Genetics:
 A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; serine/threonine-specific protein kinase
F;265-518/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
|||||
Db 404 VKIGDFGLAT 413

RESULT 13

TVTRRR
protein kinase (EC 2.7.1.37) raf - rat
N;Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: B26126
R;Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A;Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A;Reference number: A26126; MUID:871172791
A;Accession: B26126
A;Molecule type: mRNA
A;Residues: 1-602 <ISH>
A;Cross-references: GB:M15428; NID:g206546; PIDN:AAAA2002.1; PID:g206547
C;Genetics:
A;Gene: raf
C;Superfamily: rat protein kinase raf; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F;301-567/Domain: protein kinase homology <KIN>
F;309-317/Region: protein kinase ATP-binding motif
F;329/Active site: Lys status predicted
F;453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
|||||
Db 436 VKIGDFGLAT 445

RESULT 14

S34130
serine/threonine-specific protein kinase PLK (EC 2.7.1.-) - human
N;Alternate names: polo-like protein kinase; protein kinase plk-1
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S34130; I38123; S61543
R;Golsteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A;Description: Cloning and characterization of a novel human protein kinase plk-1 a pote
hrough mitosis.

A;Reference number: S34130
A;Accession: S34130
A;Molecule type: mRNA
A;Residues: 1-603 <COL>

A;Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51837.1; PID:g312998
A;Experimental source: nasopharyngeal carcinoma
R;Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.; St
proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A;Title: Induction and down-regulation of PLK, a human serine/threonine kinase expressed
A;Reference number: A53134; MUID:94173904

A;Accession: I38123
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>
A;Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769

A;Experimental source: lung tumor
R;Brauninger, A.; Strehardt, K.; Ruebsamen-Waigmann, H.

Oncogene 11, 1793-1800, 1995
A;Title: Identification and functional characterization of the human and murine polo-
A;Reference number: S61543; MUID:96068906

A;Accession: S61543
A;Molecule type: DNA

A;Residues: 1-122, 'T', 124-136 <BRA>
A;Cross-references: EMBL:X90725; NID:g1061143; PIDN:CAA62260.1; PID:g1061144
A;Experimental source: placenta

A;Note: the authors translated the codon AGC for residue 107 as Met
C;Genetics:

A;Gene: GDB:PLK
A;Cross-references: GDB:331003
A;Map position: 17pter-17p12

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;51-305/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 603;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
|||||
Db 190 VKIGDFGLAT 199

RESULT 15

A47545
protein kinase (EC 2.7.1.37) plk - mouse
C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47545
R;Clay, F.J.; McEwen, S.J.; Bertoncello, I.; Wilks, A.F.; Dunn, A.R.

proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
A;Title: Identification and cloning of a protein kinase-encoding mouse gene, Plk, rel

A;Reference number: A47545; MUID:93281660
A;Accession: A47545
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-603 <CLA>

A;Cross-references: GB:L06144; NID:g309461; PIDN:AAA39948.1; PID:g309462
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; phosphotransferase
F;51-305/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 603;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
|||||
Db 190 VKIGDFGLAT 199

Search completed: October 22, 2001, 01:28:08
Job time: 244 sec
